AMENDMENTS TO THE SPECIFICATION

In the Specification:

Please amend the paragraph on page 27, lines 15-18 as follows:

"There are several thousands of MHC genes, some of which were cloned. Table 5 below associates the MHC genes into classes and types (6). The sequences of the known MHC genes can be found in the Kabat database (http://worldwidewebimmuno-dot-bme-dot-nwu-dot-edu/)."

Please amend the paragraph on page 51, lines 5-25 as follows:

"The MHC bound peptides were resolved by reverse-phase HPLC on a 0.1 ID fused silica capillaries with length of about 30 cm (J&W) slurry packed with POROS 10 R2 (PerSepetive Biosystems). The capillaries were fitted with electrospray needle made from 36-gauge stainless tubing (Small Parts Inc. Miami Lakes, FL). A Rheodyne 9125 HPLC injector fitted with a 20 μl loop was used for loading the column. The peptides were resolved by a relatively long (90 minutes) linear gradient of 5 to 50 % acetonitrile with 0.1 % acetic acid, at a flow rate of about 1 μl/minute. The flow was electrosprayed directly from the HPLC column into an ion trap mass spectrometer (LCQ, Finnigan). The mass spectrometry analysis was done in the positive ion mode, using repetitively a full MS scan usually between 450 to 1500 atomic mass units (amu) followed by collision-induced decomposition (CID) of the dominant ion selected from the previous MS scan. In some cases the full MS was performed with a narrower mass range to reduce the number of detected peptides. The peptides were identified by comparing their MS and CID data to the calculated MS and CID of the proteins in the Genpept databank (worldwidewebwww-dot-ncbi-dot-nlm-dot nih-dotgov/genpep) using the Sequest software [25] (obtained from Finnigan, San Jose, CA). The number of times each peptide was fragmented by CID was usually limited to two by dynamic exclusion, a feature of the Xcalibur control software the LCQ mass spectrometer (Finnigan)".